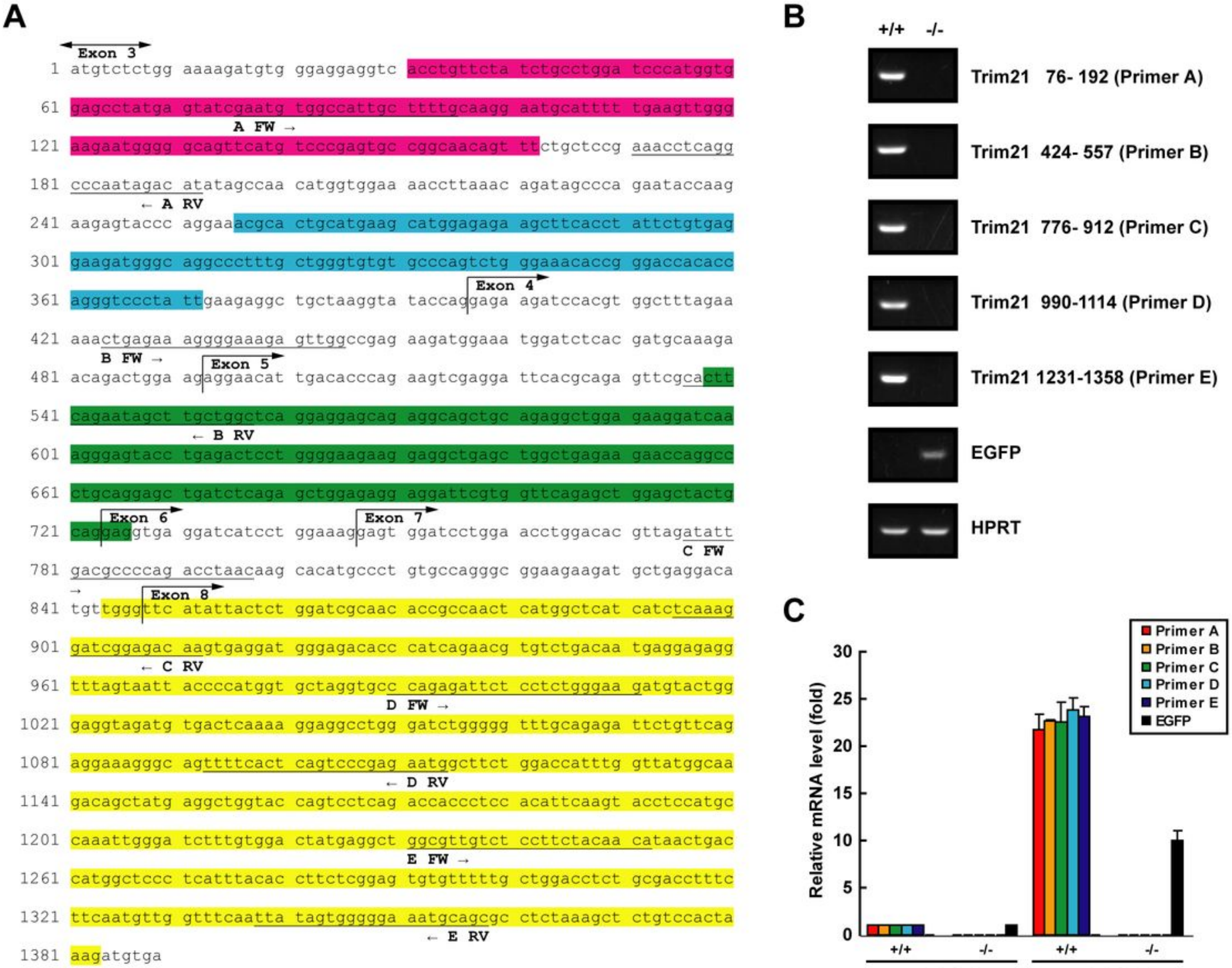
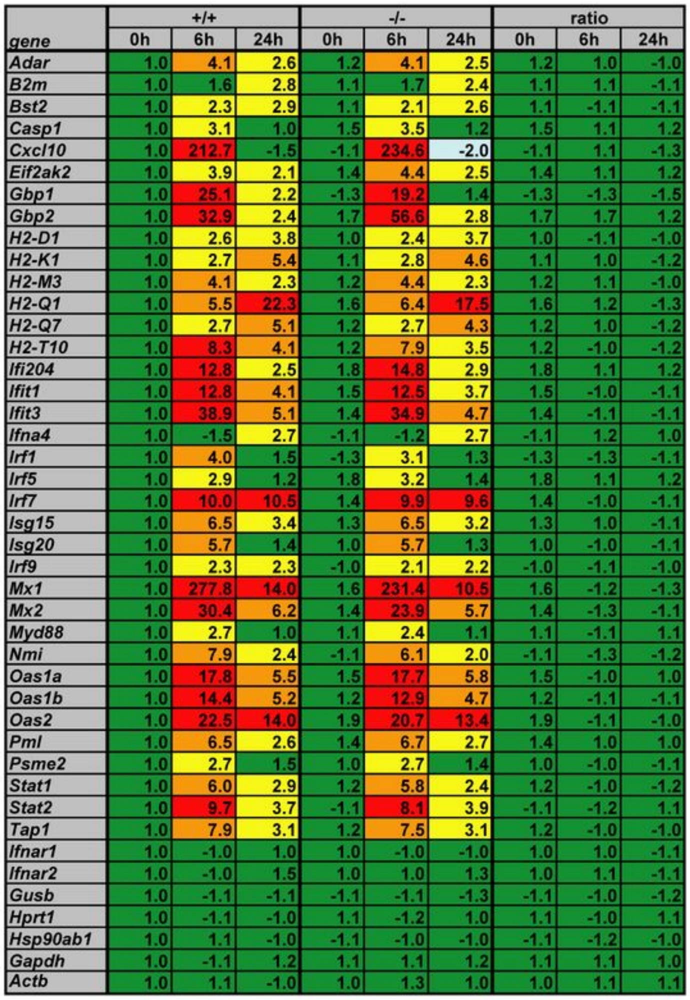


SUPPLEMENTAL FIGURE 1. The absence of Trim21 transcripts in *Trim21*$^{-/-}$ cells. *A*, Mouse Trim21 mRNA sequence (NM_009277.3) from start to stop codon. Conserved domains are highlighted with pink (RING), blue (B-box), green (coiled-coil) and yellow color (PRY/SPRY). Positions of individual exons are marked. Primers used in B and C are indicated as underlined sequences. *B*, IFN-γ-primed *Trim21*$^{+/+}$ and *Trim21*$^{-/-}$ BMMs were stimulated with poly(I:C) for 12 h, and expression of Trim21 transcripts corresponding to indicated primer sets was detected by RT-PCR. Expression of EGFP and hypoxanthine phosphoribosyltransferase (HPRT) was tested as controls. *C*, IFN-γ-primed *Trim21*$^{+/+}$ and *Trim21*$^{-/-}$ BMMs were stimulated with poly(I:C) for 12 h and levels of Trim21 transcripts detected by indicated primer sets and EGFP transcript were quantified by qPCR.

A

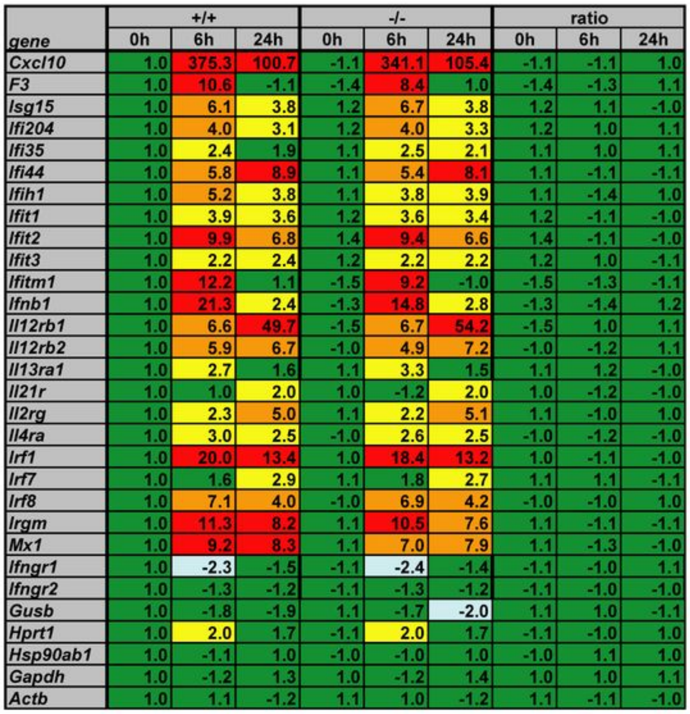
EF with IFN-β



gene	+/+			-/-			ratio		
	0h	6h	24h	0h	6h	24h	0h	6h	24h
Adar	1.0	4.1	2.6	1.2	4.1	2.5	1.2	1.0	-1.0
B2m	1.0	1.6	2.8	1.1	1.7	2.4	1.1	1.1	-1.1
Bst2	1.0	2.3	2.9	1.1	2.1	2.6	1.1	-1.1	-1.1
Casp1	1.0	3.1	1.0	1.5	3.5	1.2	1.5	1.1	1.2
Cxcl10	1.0	212.7	-1.5	-1.1	234.6	-2.0	-1.1	1.1	-1.3
Eif2ak2	1.0	3.9	2.1	1.4	4.4	2.5	1.4	1.1	1.2
Gbp1	1.0	25.1	2.2	-1.3	19.2	1.4	-1.3	-1.3	-1.5
Gbp2	1.0	32.9	2.4	1.7	56.6	2.8	1.7	1.7	1.2
H2-D1	1.0	2.6	3.8	1.0	2.4	3.7	1.0	-1.1	-1.0
H2-K1	1.0	2.7	5.4	1.1	2.8	4.6	1.1	1.0	-1.2
H2-M3	1.0	4.1	2.3	1.2	4.4	2.3	1.2	1.1	-1.0
H2-Q1	1.0	5.5	22.3	1.6	6.4	17.5	1.6	1.2	-1.3
H2-Q7	1.0	2.7	5.1	1.2	2.7	4.3	1.2	1.0	-1.2
H2-T10	1.0	8.3	4.1	1.2	7.9	3.5	1.2	-1.0	-1.2
Ifi204	1.0	12.8	2.5	1.8	14.8	2.9	1.8	1.1	1.2
Ifit1	1.0	12.8	4.1	1.5	12.5	3.7	1.5	-1.0	-1.1
Ifit3	1.0	38.9	5.1	1.4	34.9	4.7	1.4	-1.1	-1.1
Ifna4	1.0	-1.5	2.7	-1.1	-1.2	2.7	-1.1	1.2	1.0
Irf1	1.0	4.0	1.5	-1.3	3.1	1.3	-1.3	-1.3	-1.1
Irf5	1.0	2.9	1.2	1.8	3.2	1.4	1.8	1.1	1.2
Irf7	1.0	10.0	10.5	1.4	9.9	9.6	1.4	-1.0	-1.1
Isg15	1.0	6.5	3.4	1.3	6.5	3.2	1.3	1.0	-1.1
Isg20	1.0	5.7	1.4	1.0	5.7	1.3	1.0	-1.0	-1.1
Irf9	1.0	2.3	2.3	-1.0	2.1	2.2	-1.0	-1.1	-1.0
Mx1	1.0	277.8	14.0	1.6	231.4	10.5	1.6	-1.2	-1.3
Mx2	1.0	30.4	6.2	1.4	23.9	5.7	1.4	-1.3	-1.1
Myd88	1.0	2.7	1.0	1.1	2.4	1.1	1.1	-1.1	1.1
Nmi	1.0	7.9	2.4	-1.1	6.1	2.0	-1.1	-1.3	-1.2
Oas1a	1.0	17.8	5.5	1.5	17.7	5.8	1.5	-1.0	1.0
Oas1b	1.0	14.4	5.2	1.2	12.9	4.7	1.2	-1.1	-1.1
Oas2	1.0	22.5	14.0	1.9	20.7	13.4	1.9	-1.1	-1.0
Pml	1.0	6.5	2.6	1.4	6.7	2.7	1.4	1.0	1.0
Psme2	1.0	2.7	1.5	1.0	2.7	1.4	1.0	-1.0	-1.1
Stat1	1.0	6.0	2.9	1.2	5.8	2.4	1.2	-1.0	-1.2
Stat2	1.0	9.7	3.7	-1.1	8.1	3.9	-1.1	-1.2	1.1
Tap1	1.0	7.9	3.1	1.2	7.5	3.1	1.2	-1.0	-1.0
Ifnar1	1.0	-1.0	1.0	1.0	-1.0	-1.0	1.0	1.0	-1.1
Ifnar2	1.0	-1.0	1.5	1.0	1.0	1.3	1.0	1.1	-1.1
Gusb	1.0	-1.1	-1.1	-1.1	-1.1	-1.3	-1.1	-1.0	-1.2
Hprt1	1.0	-1.1	-1.0	1.1	-1.2	1.0	1.1	-1.0	1.1
Hsp90ab1	1.0	1.1	-1.0	-1.1	-1.0	-1.0	-1.1	-1.2	-1.0
Gapdh	1.0	-1.1	1.2	1.1	1.1	1.2	1.1	1.1	1.0
Actb	1.0	1.1	-1.0	1.0	1.3	1.0	1.0	1.1	1.1

B

BMM with IFN-γ



gene	+/+			-/-			ratio		
	0h	6h	24h	0h	6h	24h	0h	6h	24h
Cxcl10	1.0	375.3	100.7	-1.1	341.1	105.4	-1.1	-1.1	1.0
F3	1.0	10.6	-1.1	-1.4	8.4	1.0	-1.4	-1.3	1.1
Isg15	1.0	6.1	3.8	1.2	6.7	3.8	1.2	1.1	-1.0
Ifi204	1.0	4.0	3.1	1.2	4.0	3.3	1.2	1.0	1.1
Ifi35	1.0	2.4	1.9	1.1	2.5	2.1	1.1	1.0	1.1
Ifi44	1.0	5.8	8.9	1.1	5.4	8.1	1.1	-1.1	-1.1
Ifih1	1.0	5.2	3.8	1.1	3.8	3.9	1.1	-1.4	1.0
Ifit1	1.0	3.9	3.6	1.2	3.6	3.4	1.2	-1.1	-1.0
Ifit2	1.0	9.9	6.8	1.4	9.4	6.6	1.4	-1.1	-1.0
Ifit3	1.0	2.2	2.4	1.2	2.2	2.2	1.2	1.0	-1.1
Ifitm1	1.0	12.2	1.1	-1.5	9.2	-1.0	-1.5	-1.3	-1.1
Ifnb1	1.0	21.3	2.4	-1.3	14.8	2.8	-1.3	-1.4	1.2
Il12rb1	1.0	6.6	49.7	-1.5	6.7	54.2	-1.5	1.0	1.1
Il12rb2	1.0	5.9	6.7	-1.0	4.9	7.2	-1.0	-1.2	1.1
Il13ra1	1.0	2.7	1.6	1.1	3.3	1.5	1.1	1.2	-1.0
Il21r	1.0	1.0	2.0	1.0	-1.2	2.0	1.0	-1.2	-1.0
Il2rg	1.0	2.3	5.0	1.1	2.2	5.1	1.1	-1.0	1.0
Il4ra	1.0	3.0	2.5	-1.0	2.6	2.5	-1.0	-1.2	-1.0
Irf1	1.0	20.0	13.4	1.0	18.4	13.2	1.0	-1.1	-1.0
Irf7	1.0	1.6	2.9	1.1	1.8	2.7	1.1	1.1	-1.1
Irf8	1.0	7.1	4.0	-1.0	6.9	4.2	-1.0	-1.0	1.0
Irgm	1.0	11.3	8.2	1.1	10.5	7.6	1.1	-1.1	-1.1
Mx1	1.0	9.2	8.3	1.1	7.0	7.9	1.1	-1.3	-1.0
Ifngr1	1.0	-2.3	-1.5	-1.1	-2.4	-1.4	-1.1	-1.0	1.1
Ifngr2	1.0	-1.3	-1.2	-1.1	-1.3	-1.2	-1.1	-1.0	-1.0
Gusb	1.0	-1.8	-1.9	1.1	-1.7	-2.0	1.1	1.0	-1.1
Hprt1	1.0	2.0	1.7	-1.1	2.0	1.7	-1.1	-1.0	1.0
Hsp90ab1	1.0	-1.1	1.0	-1.0	-1.0	1.0	-1.0	1.1	1.0
Gapdh	1.0	-1.2	1.3	1.0	-1.2	1.4	1.0	1.0	1.1
Actb	1.0	1.1	-1.2	1.1	1.0	-1.2	1.1	-1.1	-1.0

🟦 x ≦ -4
⬜ -4 < x ≦ -2
🟩 -2 < x < 2
🟨 2 ≦ x < 4
🟧 4 ≦ x < 8
🟥 8 ≦ x

SUPPLEMENTAL FIGURE 2. IFN-inducible gene induction in *Trim21*$^{+/+}$ and *Trim21*$^{-/-}$ cells stimulated with IFN. *A*, *Trim21*$^{+/+}$ and *Trim21*$^{-/-}$ EFs were stimulated with IFN-β, and mRNA of type I IFN-inducible genes was quantified by PCR Array. Data shows the fold as compared to *Trim21*$^{+/+}$ values at 0 h (+/+ columns and -/- columns) or ratio between *Trim21*$^{+/+}$ and *Trim21*$^{-/-}$ at the same time point (ratio columns). Positive values indicate up-regulation while negative values demonstrate downregulation. *Ifnar1* and *Ifnar2* indicate that there is no difference in type I IFN receptor expression between *Trim21*$^{+/+}$ and *Trim21*$^{-/-}$ EFs. *Gusb*, *Hprt1*, *Hsp90ab1*, *Gapdh* and *Actb* were used as controls. Values are the means of two independent experiments. *B*, *Trim21*$^{+/+}$ and *Trim21*$^{-/-}$ unprimed BMMs were stimulated with IFN-γ, and mRNA of type II IFN-inducible genes was quantified by PCR Array. *Ifngr1* and *Ifngr2* indicate that there is no difference in type II IFN receptor expression between *Trim21*$^{+/+}$ and *Trim21*$^{-/-}$ BMMs.

SUPPLEMENTAL TABLE I. Frequency of cell populations in lymphoid organs of *Trim21*$^{+/+}$ and *Trim21*$^{-/-}$ mice

Tissue	Subset	Surface marker	Cell frequency (%)[a]	
			Trim21$^{+/+}$	*Trim21*$^{-/-}$
Thymus	Double-negative thymocyte	CD4^{-}CD8^{-}	7.91 ± 0.35	9.30 ± 0.56
	Double-positive thymocyte	CD4^{+}CD8^{+}	62.10 ± 2.01	60.98 ± 2.35
	CD4^{+} thymocyte	CD4^{+}CD8^{-}	26.98 ± 1.99	26.20 ± 2.49
	CD8^{+} thymocyte	CD4^{-}CD8^{+}	3.02 ± 0.28	3.55 ± 0.27
Bone marrow	Early pro-B cell	B220^{low}IgM^{-}CD43^{+}CD24^{-}	3.72 ± 0.09	3.20 ± 0.20
	Late pro-B/large pre-B cell	B220^{low}IgM^{-}CD43^{+}CD24^{+}	4.45 ± 0.44	4.10 ± 0.47
	Small pre-B cell	B220^{low}IgM^{-}CD43^{-}CD24^{+}	22.01 ± 1.56	22.68 ± 0.49
	Immature B cell	B220^{low}IgM^{+}	13.07 ± 0.88	15.56 ± 0.82
	Mature B cell	B220^{high}IgM^{+}	14.97 ± 2.10	15.73 ± 1.27
Spleen	B cell	CD19^{+}B220^{+}	34.20 ± 3.06	42.35 ± 2.35
	B-1a B cell	CD19^{+}CD5^{+}	3.03 ± 0.35	2.82 ± 0.19
	Plasma cell	CD138^{+}	1.51 ± 0.14	1.25 ± 0.14
	CD4^{+} T cell	CD3^{+}CD4^{+}CD8^{-}	25.64 ± 1.32	22.73 ± 1.53
	CD8^{+} T cell	CD3^{+}CD4^{-}CD8^{+}	15.13 ± 1.65	12.12 ± 1.40
	CD25^{+} regulatory T cell	CD4^{+}CD25^{+}	2.19 ± 0.24	2.15 ± 0.07
	Natural killer cell	NK-1.1^{+}CD3^{-}	3.77 ± 0.18	4.31 ± 0.42
	Macrophage	CD11b^{+}F4/80^{+}	2.80 ± 0.40	2.79 ± 0.92
	Granulocyte	CD11b^{+}F4/80^{-}Gr-1^{high}	0.68 ± 0.12	0.52 ± 0.11
	Conventional dendritic cell	CD11c^{+}B220^{-}CD19^{-}	3.14 ± 0.28	3.19 ± 0.36
	Plasmacytoid dendritic cell	CD11c^{+}B220^{+}CD19^{-}	0.94 ± 0.06	0.95 ± 0.10
Lymph node	B cell	CD19^{+}B220^{+}	18.33 ± 1.01	20.28 ± 3.74
	Plasma cell	CD138^{+}	0.78 ± 0.12	0.60 ± 0.13
	CD4^{+} T cell	CD3^{+}CD4^{+}CD8^{-}	33.32 ± 2.80	35.77 ± 2.39
	CD8^{+} T cell	CD3^{+}CD4^{-}CD8^{+}	20.44 ± 1.16	18.54 ± 2.43
	CD25^{+} regulatory T cell	CD4^{+}CD25^{+}	3.63 ± 0.32	4.01 ± 0.12
	Natural killer cell	NK-1.1^{+}CD3^{-}	1.16 ± 0.13	1.38 ± 0.16
	Macrophage	CD11b^{+}F4/80^{+}	0.91 ± 0.12	0.72 ± 0.06
	Granulocyte	CD11b^{+}F4/80^{-}Gr-1^{high}	0.03 ± 0.01	0.02 ± 0.01
	Conventional dendritic cell	CD11c^{+}B220^{-}CD19^{-}	1.43 ± 0.22	1.15 ± 0.22
	Plasmacytoid dendritic cell	CD11c^{+}B220^{+}CD19^{-}	0.39 ± 0.07	0.35 ± 0.08

[a] Mean percentage ± SEM is given for groups of 2 to 4 mice analyzed.